(1)   GENERAL INFORMATION:
      (i)   APPLICANTS:Knuth, Alexader; Jager, Elke; Chen, Yao,
                  Canlan, Matt; Gure, Ali, Old, Lloyd, Ritter, Gerd

      (ii) TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
            AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
            MHC CLASS I AND MHC CLASS II MOLECULES, AND
            USES THEREOF

      (iii) NUMBER OF SEQUENCES: 14

      (iv) CORRESPONDENCE ADDRESS:
            (A) ADDRESSEE: FULBRIGHT & JAWORSKI LLP
            (B) STREET: 666 Fifth Avenue
            (C) CITY: New York City
            (D) STATE: New York
            (E) USA
            (F) ZIP: 10158

      (v)   COMPUTER READABLE FORM:
            (A) MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
            (B) COMPUTER: IBM
            (C) OPERATING SYSTEM: PC-DOS
            (D) SOFTWARE: WordPerfect

      (vi) CURRENT APPLICATION DATA:
            (A) APPLICATION NUMBER: 09/062,422
            (B) FILING DATE: October 2, 1998
            (C) CLASSIFICATION: 530

      (vii) PRIOR APPLICATION DATA:
            (A)APPLICATION NUMBER: 08/937,263
            (B)FILING DATE: April 17, 1998

      (vii) PRIOR APPLICATION DATA:
            (A) APPLICATION NUMBER: 08/937,263
            (B) FILING DATE: September 15, 1997

      (vii) PRIOR APPLICATION DATA:
            (A) APPLICATION NUMBER: US 08/752,182
            (B) FILING DATE: 03-October-1996

      (viii) ATTORNEY/AGENT INFORMATION:
            (A) NAME: Hanson, Norman D.
            (B) REGISTRATION NUMBER: 30,946
            (C) REFERENCE/DOCKET NUMBER: LUD 5466.3

      (ix) TELECOMMUNICATION INFORMATION:
            (A) TELEPHONE: (212) 688-9200
            (B) TELEFAX: (212) 838-3884

(2)   INFORMATION FOR SEQ ID NO: 1:
         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 752 base pairs
              (B) TYPE: nuclear acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATCCTCGTGG GCCCTGACCT TCTCTCTGAG AGCCGGGCAG AGGCTCCGGA GCC   53

ATG CAG GCC GAA GGC CGG GGC ACA GGG GGT TCG ACG GGC GAT GCT   98
Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala
                  5   10   15

GAT GGC CCA GGA GGC CCT GGC ATT CCT GAT GGC CCA GGG GGC AAT   143
Asp Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn
                 20   25   30

GCT GGC GGC CCA GGA GAG GCG GGT GCC ACG GGC GGC AGA GGT CCC   188
Ala Gly Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Aly Pro
                 35   40   45

CGG GGC GCA GGG GCA GCA AGG GCC TCG GGG CCG GGA GGA GGC GCC   233
Arg Gly Ala Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala
                 50   55   60

CCG CGG GGT CCG CAT GGC GGC GCG GCT TCA GGG CTG AAT GGA TGC   278
Pro Arg Gly Pro His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys
                 65   70   75

TGC AGA TGC GGG GCC AGG GGG CCG GAG AGC CGC CTG CTT GAG TTC   323
Cys Arg Cys Gly Ala Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe
                 80   80   90

TAC CTC GCC ATG CCT TTC GCG ACA CCC ATG GAA GCA GAG CTG GCC   368
Tyr Leu Ala Met Pro Phe Ala Thr Pro Met Glu Ala Glu Leu Ala
                 95   100   105

CGC AGG AGC CTG GCC CAG GAT GCC CCA CCG CTT CCC GTG CCA GGG   413
Arg Arg Ser Leu Ala Gln Asp Ala Pro Pro Leu Pro Val Pro Gly
                110   115   120

GTG CTT CTG AAG GAG TTC ACT GTG TCC GGC AAC ATA CTG ACT ATC   458
Val Leu Leu Lys Glu Phe Thr Val Ser Gly Asn Ile Leu Thr Ile
                125   130   135

CGA CTG ACT GCT GCA GAC CAC CGC CAA CTG CAG CTC TCC ATC AGC   503
Arg Leu Thr Ala Ala Asp His Arg Gln Leu Gln Leu Ser Ile Ser
                140   145   150

TCC TGT CTC CAG CAG CTT TCC CTG TTG ATG TGG ATC ACG CAG TGC   548
Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp Ile Thr Gln Cys
                155   160   165

```
TTT CTG CCC GTG TTT TTG GCT CAG CCT CCC TCA GGG CAG AGG CGC          593
Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser Gly Gln Arg Arg
                170                 175                 180


TAA GCCCAGCCTG GCGCCCCTTC CTAGGTCATG CCTCCTCCCC TAGGGAATGG          646
TCCCAGCACG AGTGGCCAGT TCATTGTGGG GGCCTGATTG TTTGTCGCTG GAGGAGGACG    706
GCTTACATGT TTGTTTCTGT AGAAAATAAA ACTGAGCTAC GAAAAA                   752
```

(2)   INFORMATION FOR SEQ ID NO: 2:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 31 base pairs
           (B) TYPE: nuclear acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
CACACAGGAT CCATGGATGC TGCAGATGCG G                                   31
```

(2)   INFORMATION FOR SEQ ID NO: 3:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 32 base pairs
           (B) TYPE: nuclear acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
CACACAAAGC TTGGCTTAGC GCCTCTGCCC TG                                  32
```

(2)   INFORMATION FOR SEQ ID NO: 4:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 11 amino acids
           (B) TYPE: amino acid
           (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
Ser Leu Leu Met Trp Ile Thr Gln Cys Phe Leu
                5                   10
```

(2)   INFORMATION FOR SEQ ID NO: 5:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 9 amino acids
           (B) TYPE: amino acid
           (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```
Ser Leu Leu Met Trp Ile Thr Gln Cys
```

(2)   INFORMATION FOR SEQ ID NO: 6:
       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 9 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Gln Leu Ser Leu Leu Met Trp Ile Thr
                5

(2)   INFORMATION FOR SEQ ID NO: 7:
       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 10 amino acids
            (B) TYPE; amino acid
            (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Leu Leu Met Trp Ile Thr Gln Cys Phe Leu
                5   10

(2)   INFORMATION FOR SEQ ID NO: 8:
       (i) SEQUENCE CHARACTERISTICS
            (A) LENGTH: 18 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ala Ala Asp His Arg Gln Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln
                5   10   15

Gln Leu

(2)   INFORMATION FOR SEQ ID NO: 9:
       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 18 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Val Leu Leu Lys Glu Phe Thr Val Ser Gly Asn Ile Leu Thr Ile Arg
                5   10   15

Leu Thr

(2)   INFORMATION FOR SEQ ID NO: 10:

```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 18 amino acids
    (B) TYPE; amino acid
    (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:


Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val Ser Gly
              5                   10                  15

Asn Ile

(2)    INFORMATION FOR SEQ ID NO: 11:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:


Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala Arg Gly
              5                   10                  15

Pro Glu


(2)    INFORMATION FOR SEQ ID NO: 12:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:


Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe Ala Thr Pro Met
              5                   10                  15

Glu Ala


(2)    INFORMATION FOR SEQ ID NO: 13:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:


Thr Val Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His
              5                   10                  15

Arg Gln
```

(2)   INFORMATION FOR SEQ ID NO: 14:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 6 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Leu Leu Met Trp Ile Thr

5